

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/358,103

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 \_\_\_\_\_ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 \_\_\_\_\_ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 \_\_\_\_\_ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 \_\_\_\_\_ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 \_\_\_\_\_ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 \_\_\_\_\_ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 \_\_\_\_\_ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
**(2) INFORMATION FOR SEQ ID NO:X:**  
**(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")**  
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
**This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 \_\_\_\_\_ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
**<210> sequence id number**  
**<400> sequence id number**  
**000**
- 10 \_\_\_\_\_ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 \_\_\_\_\_ Use of <213>Organism (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.
- 12 \_\_\_\_\_ Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
**Please explain source of genetic material in <220> to <223> section.**  
**(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)**
- 13 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.  
  
AKS-Biotechnology Systems Branch- 5/15/99

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/358,103DATE: 07/30/1999  
TIME: 12:05:22

Input Set: I358103.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

Does Not Comply  
Corrected Diskette Needed

1 <110> APPLICANT: Roca, Alberto I  
2 <120> TITLE OF INVENTION: Mutants of Maw Motifs of RecA Protein Homologs, Methods  
3 of Making Them, and Their Uses  
4 <130> FILE REFERENCE: RecA Homolog Protein & Mutants  
5 <140> CURRENT APPLICATION NUMBER: US/09/358,103  
6 <141> CURRENT FILING DATE: 1999-07-21  
7 <150> EARLIER APPLICATION NUMBER: 60/094,071  
8 <151> EARLIER FILING DATE: 1998-07-24  
9 <160> NUMBER OF SEQ ID NOS: 3  
10 <170> SOFTWARE: PatentIn Ver. 2.0  
11 <210> SEQ ID NO 1  
12 <211> LENGTH: 26  
13 <212> TYPE: PRT  
14 <213> ORGANISM: Escherichia coli  
15 <220> FEATURE:  
16 <221> NAME/KEY: NON\_TER  
17 <222> LOCATION: (1)  
18 <220> FEATURE:  
19 <221> NAME/KEY: NON\_TER  
20 <222> LOCATION: (26)..)  
21 <220> FEATURE:  
22 <221> NAME/KEY: HELIX  
23 <222> LOCATION: (6)..(12)  
24 <223> OTHER INFORMATION: Alpha-helix B  
25 <220> FEATURE:  
26 <221> NAME/KEY: STRAND  
27 <222> LOCATION: (22)..(26)  
28 <223> OTHER INFORMATION: Beta-strand 1  
29 <220> FEATURE:  
30 <221> NAME/KEY: SIMILAR  
31 <222> LOCATION: (1)..(26)  
32 <223> OTHER INFORMATION: This structure is highly conserved across  
33 bacterial RecA and homologous eukaryotic,  
34 archaeal, and viral proteins; sequence below is  
35 from E. coli RecA positions 40-65  
36 <400> SEQUENCE: 1  
37 Ile Ser Thr Gly Ser Leu Ser Leu Asp Ile Ala Leu Gly Ala Gly Gly  
38 1 5 10 15  
39 Leu Pro Met Gly Arg Ile Val Glu Ile Tyr  
40 20 25  
41 <210> SEQ ID NO 2  
42 <211> LENGTH: 26  
43 <212> TYPE: PRT  
44 <213> ORGANISM: Escherichia coli

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45      <220> FEATURE:
46      <221> NAME/KEY: NON_TER
47      <222> LOCATION: (1)
48      <220> FEATURE:
49      <221> NAME/KEY: NON_TER
50      <222> LOCATION: (26)
51      <220> FEATURE:
52      <221> NAME/KEY: HELIX
53      <222> LOCATION: (6)..(12)
54      <223> OTHER INFORMATION: Alpha-helix B
55      <220> FEATURE:
56      <221> NAME/KEY: STRAND
57      <222> LOCATION: (22)..(26)
58      <223> OTHER INFORMATION: Beta-strand 1
59      <220> FEATURE:
60      <221> NAME/KEY: SIMILAR
61      <222> LOCATION: (1)..(26)
62      <223> OTHER INFORMATION: Non 'Xaa' residues are the invariant MAW-motif
63      residues in RecA and its homologs
64      <400> SEQUENCE: 2

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*what about the Xaa's*

W--v 65 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly  
66 15  
W-- 67 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa  
68 20 25

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69 <210> SEQ ID NO 3
70 <211> LENGTH: 26
71 <212> TYPE: PRT
72 <213> ORGANISM: Escherichia coli
73 <220> FEATURE:
74 <221> NAME/KEY: NON_TER
75 <222> LOCATION: (1)
76 <220> FEATURE:
77 <221> NAME/KEY: NON_TER
78 <222> LOCATION: (26)
79 <220> FEATURE:
80 <221> NAME/KEY: HELIX
81 <222> LOCATION: (6)..(12)
82 <223> OTHER INFORMATION: Alpha-helix B
83 <220> FEATURE:
84 <221> NAME/KEY: STRAND
85 <222> LOCATION: (22)..(26)
86 <223> OTHER INFORMATION: Beta-strand 1
87 <220> FEATURE:
88 <221> NAME/KEY: SIMILAR
89 <222> LOCATION: (1)..(26)

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90 <223> OTHER INFORMATION: Non "Xaa" residues are the invariant and  
91 semiconservative elements of the MAW motif in RecA  
92 and its homologs *same error*

93 <400> SEQUENCE: 3  
W-- 94 Ile Xaa Thr Gly Xaa Xaa Xaa Leu Asp Xaa Ala Leu Xaa Xaa Gly Gly

what about the Xaa's? They need to be defined (see item 10 or Even summary sheet)

in RecA  
same error as above

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/358,103

DATE: 07/30/1999  
TIME: 12:05:22

Input Set: I358103.RAW

	95		1						10		15
W-->	96	Leu	Xaa	Xaa	Gly	Xaa	Ile	Val	Glu	Ile	Tyr
	97				20				25		

VERIFICATION SUMMARY  
PATENT APPLICATION US/09/358,103DATE: 07/30/1999  
TIME: 12:05:22

Input Set: I358103.RAW

Line	Error/Warning	Original Text
65	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
67	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa
94	W "N" or "Xaa" used: Feature required	Ile Xaa Thr Gly Xaa Xaa Xaa Leu Asp Xaa A
96	W "N" or "Xaa" used: Feature required	Leu Xaa Xaa Gly Xaa Ile Val Glu Ile Tyr